WHAT IS CLAIMED IS:

1. A computer-implemented method of presenting expression level information as collected from first and second samples, said method comprising the steps of:

displaying a first axis corresponding to expression level in said first sample;

displaying a second axis substantially perpendicular to said first axis, said second axis corresponding to expression level in said second sample; and

for a selected expressed sequence, displaying a mark at a position, wherein said position is selected relative to said first axis in accordance with an expression level of said selected expressed sequence in said first sample and relative to said second axis in accordance with an expression level of said selected expressed sequence in said second sample.

2. The method of claim 1 wherein said selected expressed sequence comprises a gene.

3. The method of claim 1 wherein said selected expressed sequence comprises a portion of a gene.

4. The method of claim 1 further comprising the step of repeating said displaying a mark step for a plurality of selected expressed sequences.

5. The method of claim 1 further comprising the steps of:

monitoring said expression level of said expressed sequence in said first sample and said second sample.

6. The method of claim 3 wherein said monitoring step for one of said samples comprises substeps of:

inputting a plurality of hybridization intensities of pairs of perfect match and mismatch probes, said perfect match probes being perfectly complementary to a target nucleic acid sequence indicative of expression of said selected gene and said mismatch probes having at least one base mismatch with said target sequence, and said

hybridization intensities indicating hybridization affinity between said perfect match and mismatch probes and a sample nucleic acid sequence from said one of said samples;

comparing the hybridization intensities of each pair of perfect match probe and mismatch probe; and

generating said expression level for said expressed sequence and said one of said samples responsive to results of said comparing step.

7. The method of claim 6 further comprising the step of:

comparing a difference between hybridization intensities of perfect match and mismatch probes at a base position to a difference threshold.

8. The method of claim 7 further comprising the step of:

comparing a quotient of hybridization intensities of perfect match and mismatch probes at a base position to a ratio threshold.

9. The method of claim 6 further comprising the steps of:

a) counting a probe pair as a positive probe pair to increment a positive probe pair count if a perfect match probe intensity minus a mismatch probe intensity exceeds a difference threshold and said perfect match probe intensity divided by said mismatch probe intensity exceeds a ratio threshold;

b) counting said probe pair as a negative probe pair to increment a negative probe pair count if said mismatch probe intensity minus said perfect match probe intensity exceeds said difference threshold and said mismatch probe intensity divided by said perfect match probe intensity exceeds said ratio threshold; and

c) computing a logarithmic ratio of said perfect match probe intensity to said mismatch probe intensity.

10. The method of claim 9 further comprising the steps of:

repeating said a), b), and c) steps for each of said probe pairs,

accumulating a sum of differences of said perfect match and mismatch probe intensities for probe pairs that cause; and

determining an expression level of said selected expressed sequence to be an average of said differences.

11. The method of claim 1 further comprising the steps of:

receiving user input selecting said mark; and

in response to said user input, displaying information about said selected expressed sequence.

12. The method of claim 11 further comprising the steps of:

in response to said user input, displaying information about said selected expressed sequence.

13. The method of claim 12 wherein said information about said selected expressed sequence comprises a GenBank accession number.

14. The method of claim 12 wherein said information about said selected expressed sequence comprises a GenBank database record for said selected expressed sequence.

15. The method of claim 1 wherein said first sample and said second sample are collected from tissue samples differing in a particular characteristic.

16. The method of claim 15 wherein said particular characteristic comprises presence of disease.

17. The method of claim 15 wherein said particular characteristic comprises a treatment strategy for a disease.

18. The method of claim 1 wherein said particular characteristic is a stage of a disease.

19. The method of claim 1 further comprising the step of :

displaying a third axis substantially perpendicular to said first axis and to said second axis in a three-dimensional display environment wherein said position of said mark is further selected relative to said third axis in accordance with an expression level of said selected expressed sequence in a third sample.

20. A computer-implemented method of presenting sample analysis information comprising the steps of:

displaying a first axis corresponding to a concentration of a compound in a first sample as determined by monitoring binding of said compound to a selected polymer having binding affinity to said compound;

displaying a second axis substantially perpendicular to said first axis, said second axis corresponding to a concentration of said compound in said second sample as determined by monitoring binding of said compound to said selected polymer; and

displaying a mark at a position, wherein said position is selected relative to said first axis in accordance with said concentration in said first sample and relative to said second axis in accordance with said concentration in said second sample.

21. The method of claim 20 wherein said selected polymer comprises a nucleic acid sequence.

22. The method of claim 20 wherein said selected polymer comprises a protein.

23. The method of claim 21 further comprising the step of:

obtaining said concentration of said compound in said first sample by exposing said first sample to a plurality of nucleic acid probes.

24. The method of claim 22 further comprising the step of:

obtaining said concentration of said compound in said first sample by exposing said first sample to a plurality of peptide probes.

25. A computer program product for presenting expression level information as collected from first and second samples, said product comprising::

code for displaying a first axis corresponding to expression level in said first sample;

code for displaying a second axis substantially perpendicular to said first axis, said second axis corresponding to expression level in said second sample;

code for, for a selected expressed sequence, displaying a mark at a

position, wherein said position is selected relative to said first axis in accordance with an expression level of said selected expressed sequence in said first sample and relative to said second axis in accordance with an expression level of said selected expressed sequence in said second sample; and

a computer-readable storage medium for storing the codes.

26. The product of claim 25 wherein said selected expressed sequence comprises a gene.

27. The product of claim 25 wherein said selected expressed sequence comprises a portion of a gene.

28. The product of claim 25 further comprising code for repeatedly applying said displaying a mark code for a plurality of selected expressed sequences.

29. The product of claim 25 further comprising:

code for monitoring said expression level of said expressed sequence in said first sample and said second sample.

30. The product of claim 27 wherein said monitoring step for one of said samples comprises:

code for inputting a plurality of hybridization intensities of pairs of perfect match and mismatch probes, said perfect match probes being perfectly complementary to a target nucleic acid sequence indicative of expression of said selected gene and said mismatch probes having at least one base mismatch with said target sequence, and said hybridization intensities indicating hybridization affinity between said perfect match and mismatch probes and a sample nucleic acid sequence from said one of said samples;

comparing the hybridization intensities of each pair of perfect match probe and mismatch probe; and

generating said expression level for said expressed sequence and said one of said samples responsive to results of said comparing step.

31. The product of claim 30 further comprising:

code for comparing a difference between hybridization intensities of perfect match and mismatch probes at a base position to a difference threshold.

32. The product of claim 31 further comprising:

code for comparing a quotient of hybridization intensities of perfect match and mismatch probes at a base position to a ratio threshold.

33. The product of claim 30 further comprising:

a) code for counting a probe pair as a positive probe pair to increment a positive probe pair count if a perfect match probe intensity minus a mismatch probe intensity exceeds a difference threshold and said perfect match probe intensity divided by said mismatch probe intensity exceeds a ratio threshold;

b) code for counting said probe pair as a negative probe pair to increment a negative probe pair count if said mismatch probe intensity minus said perfect match probe intensity exceeds said difference threshold and said mismatch probe intensity divided by said perfect match probe intensity exceeds said ratio threshold; and

c) code for computing a logarithmic ratio of said perfect match probe intensity to said mismatch probe intensity.

34. The product of claim 33 further comprising:

code for repeatedly applying said a), b), and c) codes for each of said probe pairs, accumulating a sum of differences of said perfect match and mismatch probe intensities for probe pairs that cause; and

code for determining an expression level of said selected expressed sequence to be an average of said differences.

35. The product of claim 25 further comprising:

code for receiving user input selecting said mark; and

code for, in response to said user input, displaying information about said selected expressed sequence.

36. The product of claim 35 further comprising:

code for, in response to said user input, displaying information about said selected expressed sequence.

37. The product of claim 36 wherein said information about said selected expressed sequence comprises a GenBank accession number.

38. The product of claim 36 wherein said information about said selected expressed sequence comprises a GenBank database record for said selected expressed sequence.

39. The product of claim 25 wherein said first sample and said second sample are collected from tissue samples differing in a particular characteristic.

40. The product of claim 39 wherein said particular characteristic comprises presence of disease.

41. The product of claim 39 wherein said particular characteristic comprises a treatment strategy for a disease.

42. The product of claim 25 wherein said particular characteristic is a stage of a disease.

43. The product of claim 25 further comprising the step of :

displaying a third axis substantially perpendicular to said first axis and to said second axis in a three-dimensional display environment wherein said position of said mark is further selected relative to said third axis in accordance with an expression level of said selected expressed sequence in a third sample.

44. A computer program product for presenting sample analysis information comprising:

code for displaying a first axis corresponding to a concentration of a compound in a first sample as determined by monitoring binding of said compound to a

selected polymer having bonding affinity to said compound;

code for displaying a second axis substantially perpendicular to said first axis, said second axis corresponding to concentration of said compound in a second sample as determined by monitoring binding of said compound to said selected polymer;

code for displaying a mark at a position, wherein said position is selected relative to said first axis in accordance with said concentration in said first sample and relative to said second axis in accordance with said concentration in said second sample; and

a computer-readable storage medium that stores the codes.

45. The product of claim 44 wherein said selected polymer comprises a nucleic acid sequence.

46. The product of claim 44 wherein said selected polymer comprises a protein.

47. A computer system comprising a display, a processor, and a memory that stores instructions for configuring said processor to:

display a first axis corresponding to expression level in said first sample;

display a second axis substantially perpendicular to said first axis, said second axis corresponding to expression level in said second sample; and

for a selected expressed sequence, display a mark at a position, wherein said position is selected relative to said first axis in accordance with an expression level of said selected expressed sequence in said first sample and relative to said second axis in accordance with an expression level of said selected expressed sequence in said second sample.

48. A computer system comprising a display, a processor, and a memory that stores instructions for configuring said processor to:

display a first axis corresponding to a concentration of a compound in a first sample as determined by monitoring binding of said compound to a selected polymer having binding affinity to said compound;

display a second axis substantially perpendicular to said first axis, said

second axis corresponding to a concentration of said compound in said second sample as determined by monitoring binding of said compound to said selected polymer; and

display a mark at a position, wherein said position is selected relative to said first axis in accordance with said concentration in said first sample and relative to said second axis in accordance with said concentration in said second sample.